

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
Goli, Surya K.

(ii) TITLE OF THE INVENTION: NOVEL CALCIUM-BINDING
PROTEIN

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
- (B) STREET: 3174 Porter Drive
- (C) CITY: Palo Alto
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 94304

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: To Be Assigned
- (B) FILING DATE: Filed Herewith
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Billings, Lucy J.
- (B) REGISTRATION NUMBER: 36,749
- (C) REFERENCE/DOCKET NUMBER: PF-0261 US

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415-855-0555
- (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: CONUTUT01
- (B) CLONE: 2509570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Met	Trp	Arg	Pro	Ser	Val	Leu	Leu	Leu	Leu	Leu	Leu	Arg	His
1				5				10					15	
Gly	Ala	Gln	Gly	Lys	Pro	Ser	Pro	Asp	Ala	Gly	Pro	His	Gly	Gln
		20						25					30	
Arg	Val	His	Gln	Ala	Ala	Pro	Leu	Ser	Asp	Ala	Pro	His	Asp	Asp
		35					40					45		
His	Gly	Asn	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu	Gly	Arg	Glu
		50					55				60			

Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu
65 70 75 80
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp
85 90 95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg
100 105 110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp
115 120 125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly
130 135 140
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr
145 150 155 160
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Phe Arg Val Ala Asp
165 170 175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu
180 185 190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr
195 200 205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu
210 215 220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala
225 230 235 240
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn
245 250 255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro
260 265 270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu
275 280 285
Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
290 295 300
Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
305 310 315 320
Leu Thr Arg His His Asp Glu Leu
325

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: CONTUT01
- (B) CLONE: 2509570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGAGAGCGGA	NGNANTGGNA	TAACAGGGGA	CCGATGATGT	GGCGACCATC	AGTTCTGCTG	60
CTTCTGTTGC	TACTGAGGCA	CGGGGCCAG	GGGAAGCCAT	CCCCAGACGC	AGGCCCTCAT	120
GGCCAGGGGA	GGGTGCACCA	GGCGGCCCC	CTGAGCGACG	CTCCCCATGA	TGACGCCCCAC	180
GGGAAC'TTCC	AGTACGACCA	TGAGGCT'TTC	CTGGGACGGG	AAGTGGCCAA	GGAATTTCGAC	240
CAACTCACCC	CAGAGGAAAG	CCAGGCCCGT	CTGGGGCGGA	TCGTGGACCG	CATGGACCGC	300
GCGGGGGACG	GCGACGGCTG	GGTGTGCTG	GCCGAGCTTC	GCGCGTGGAT	GCAGCACACG	360
CAGCAGCGGC	ACATACGGGA	CTCGGTGAGC	GCGGCTGGG	ACACGTACGA	CACGGACCGC	420
GACGGGCGTG	TGGGTTGGGA	GGAGCTGCGC	AACGCCACCT	ATGGCCACTA	CGCGCCCGGT	480
GAAGAATTTC	ATGACGTGGA	GGATGCAGAG	ACCTACAAAA	AGATGCTGGC	TCGGGACGAG	540
CGGCGTTTCC	GGGTGGCCGA	CCAGGATGGG	GACTCGATGG	CCACTCGAGA	GGAGCTGACA	600
GCCTTCCTGC	ACCCCGAGGA	GTTCCCTCAC	ATGCGGGACA	TCGTGATTGC	TGAAACCCTG	660
GAGGACCTGG	ACAGAAACAA	AGATGGCTAT	GTCCAGGTGG	AGGAGTACAT	CGCGGATCTG	720
TACTCAGCCG	AGCCTGGGGA	GGAGGAGCCG	GCGTGGGTGC	AGACGGAGAG	GCAGCAGTTC	780
CGGGACTTCC	GGGATCTGAA	CAAGGATGGG	CACCTGGATG	GGAGTGAGGT	GGGCCACTGG	840
GTGCTGCCCC	CTGCCAGGA	CCAGCCCCTG	GTGGAAGCCA	ACCACCTGCT	GCACGAGAGC	900
GACACGGACA	AGGATGGGCG	GCTGAGCAAA	GCGGAAATCC	TGGGTAATTG	GAACATGTTT	960
GTGGGCAGTC	AGGCCACCAA	CTATGGCGAG	GACCTGACCC	GGCACCACGA	TGAGCTGTGA	1020

GCACCGCGCA CCTGCCACAG CCTCAGAGGC CCGCA

1055

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1262329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ala Arg Gly Gly Arg Gly Arg Arg Leu Gly Leu Ala Leu Gly Leu
 1 5 10 15
 Leu Leu Ala Leu Val Leu Ala Pro Arg Val Leu Arg Ala Lys Pro Thr
 20 25 30
 Val Arg Lys Glu Arg Val Val Arg Pro Asp Ser Glu Leu Gly Glu Arg
 35 40 45
 Pro Pro Glu Asp Asn Gln Ser Phe Gln Tyr Asp His Glu Ala Phe Leu
 50 55 60
 Gly Lys Glu Asp Ser Lys Thr Phe Asp Gln Leu Thr Pro Asp Glu Ser
 65 70 75 80
 Lys Glu Arg Leu Gly Lys Ile Val Asp Arg Ile Asp Asn Asp Gly Asp
 85 90 95
 Gly Phe Val Thr Thr Glu Glu Leu Lys Thr Trp Ile Lys Arg Val Gln
 100 105 110
 Lys Arg Tyr Ile Phe Asp Asn Val Ala Lys Val Trp Lys Asp Tyr Asp
 115 120 125
 Arg Asp Lys Asp Asp Lys Ile Ser Trp Glu Glu Tyr Lys Gln Ala Thr
 130 135 140
 Tyr Gly Tyr Tyr Leu Gly Asn Pro Ala Glu Phe His Asp Ser Ser Asp
 145 150 155 160
 His His Thr Phe Lys Lys Met Leu Pro Arg Asp Glu Arg Arg Phe Lys
 165 170 175
 Ala Ala Asp Leu Asn Gly Asp Leu Thr Ala Thr Arg Glu Glu Phe Thr
 180 185 190
 Ala Phe Leu His Pro Glu Glu Phe Glu His Met Lys Glu Ile Val Val
 195 200 205
 Leu Glu Thr Leu Glu Asp Ile Asp Lys Asn Gly Asp Gly Phe Val Asp
 210 215 220
 Gln Asp Glu Tyr Ile Ala Asp Met Phe Ser His Glu Glu Asn Gly Pro
 225 230 235 240
 Glu Pro Asp Trp Val Leu Ser Glu Arg Glu Gln Phe Asn Glu Phe Arg
 245 250 255
 Asp Leu Asn Lys Asp Gly Lys Leu Asp Lys Asp Glu Ile Arg His Trp
 260 265 270
 Ile Leu Pro Gln Asp Tyr Asp His Ala Gln Ala Glu Ala Arg His Leu
 275 280 285
 Val Tyr Glu Ser Asp Lys Asn Lys Asp Glu Lys Leu Thr Lys Glu Glu
 290 295 300
 Ile Leu Glu Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr
 305 310 315 320
 Gly Glu Asp Leu Thr Lys Asn His Asp Glu Leu
 325 330

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 220582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Arg Gly Gly Arg Leu Gly Leu Ala Leu Gly Leu Leu Leu Ala
 1 5 10 15
 Leu Val Leu Ala Leu Arg Ala Lys Pro Thr Val Arg Lys Glu Arg Val
 20 25 30
 Val Arg Pro Asp Ser Glu Leu Gly Glu Arg Pro Pro Glu Asp Asn Gln
 35 40 45
 Ser Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Lys Glu Asp Ser Lys
 50 55 60
 Thr Phe Asp Gln Leu Ser Pro Asp Glu Ser Lys Glu Arg Leu Gly Lys
 65 70 75 80
 Ile Val Asp Arg Ile Asp Ser Asp Gly Asp Gly Leu Val Thr Thr Glu
 85 90 95
 Glu Leu Lys Leu Trp Ile Lys Arg Val Gln Lys Arg Tyr Ile Tyr Asp
 100 105 110
 Asn Val Ala Lys Val Trp Lys Asp Tyr Asp Arg Asp Lys Asp Glu Lys
 115 120 125
 Ile Ser Trp Glu Glu Tyr Lys Gln Ala Thr Tyr Gly Tyr Tyr Leu Gly
 130 135 140
 Asn Pro Ala Glu Phe His Asp Ser Ser Asp His Thr Phe Lys Lys
 145 150 155 160
 Met Leu Pro Arg Asp Glu Arg Arg Phe Lys Ala Ser Asp Leu Asp Gly
 165 170 175
 Asp Leu Thr Ala Thr Arg Glu Glu Phe Thr Ala Phe Leu His Pro Glu
 180 185 190
 Glu Phe Glu His Met Lys Glu Ile Val Val Leu Glu Thr Leu Glu Asp
 195 200 205
 Ile Asp Lys Asn Gly Asp Gly Phe Val Asp Gln Asp Glu Tyr Ile Ala
 210 215 220
 Asp Met Phe Ser His Glu Asp Asn Gly Pro Glu Pro Asp Trp Val Leu
 225 230 235 240
 Ser Glu Arg Glu Gln Phe Asn Asp Phe Arg Asp Leu Asn Lys Asp Gly
 245 250 255
 Lys Leu Asp Lys Asp Glu Ile Arg His Trp Ile Leu Pro Gln Asp Tyr
 260 265 270
 Asp His Ala Gln Ala Glu Ala Arg His Leu Val Tyr Glu Ser Asp Lys
 275 280 285
 Asn Lys Asp Glu Met Leu Thr Lys Glu Glu Ile Leu Asp Asn Trp Asn
 290 295 300
 Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp Leu Thr Lys
 305 310 315 320
 Asn His Asp Glu Leu
 325

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